



SEQUENCE LISTING

<110> Quinnan, Gerald V.
Zhang, Peng Fei

<120> Expression and Characterization of HIV-1 Envelope
Protein Associated with a Broadly Reactive Neutralizing
Antibody Response

<130> 44508-5001-US

<140> US 09/762,261

<141> 2001-02-05

<150> US 60/095,267

<151> 1998-08-04

<150> PCT/US99/17596

<151> 1999-08-04

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 866

<212> PRT

<213> Human immunodeficiency virus type 1

<220>

<223> R2 strain envelope protein (gp 160)

<400> 1

Met Arg Val Lys Gly Ile Arg Arg Asn Tyr Gln His Trp Trp Gly Trp
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Gly Thr Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Thr Glu Lys
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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Val Glu Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
 115 120 125

Asn Cys Thr Asp Leu Arg Asn Thr Thr Asn Thr Asn Asn Ser Thr Asp
 130 135 140

Asn Asn Asn Ser Asn Ser Glu Gly Thr Ile Lys Gly Gly Glu Met Lys
 145 150 155 160

Asn Cys Ser Phe Asn Ile Ala Thr Ser Ile Gly Asp Lys Met Gln Lys
 165 170 175

Glu Tyr Ala Leu Leu Tyr Lys Leu Asp Ile Glu Pro Ile Asp Asn Asp
 180 185 190

Asn Thr Ser Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
 195 200 205

Ala Cys Pro Lys Ile Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
 210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Ser Gly
 225 230 235 240

Lys Gly Ser Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
 245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
 260 265 270

Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr
 275 280 285

Ile Ile Val Gln Leu Arg Glu Pro Val Lys Ile Asn Cys Ser Arg Pro
 290 295 300

Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe
 305 310 315 320

Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
 325 330 335

Ile Ser Lys Thr Asn Trp Thr Asn Ala Leu Lys Gln Val Val Glu Lys
 340 345 350

Leu Gly Glu Gln Phe Asn Lys Thr Lys Ile Val Phe Thr Asn Ser Ser
 355 360 365

Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Ala Gly Glu
 370 375 380

Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asp Ser Ile Trp Asn Ser
 385 390 395 400

Glu Asn Gly Thr Trp Asn Ile Thr Arg Gly Leu Asn Asn Thr Gly Arg
 405 410 415

Asn Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg
 420 425 430

Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Lys Gly Asn
 435 440 445

Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
 450 455 460

Gly Lys Asp Asp Asn Ser Arg Asp Gly Asn Glu Thr Phe Arg Pro Gly
 465 470 475 480

Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys
 485 490 495

Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg
 500 505 510

Arg Val Val Gln Arg Glu Glu Arg Ala Val Gly Leu Gly Ala Met Phe
 515 520 525

Phe Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Val
 530 535 540

Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln
 545 550 555 560

Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
 565 570 575

Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val
 580 585 590

Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
 595 600 605

Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser
 610 615 620

Lys Asn Lys Thr Leu Glu Ala Ile Trp Asn Asn Met Thr Trp Met Gln
 625 630 635 640

Trp Asp Lys Glu Ile Asp Asn Tyr Thr Ser Leu Ile Tyr Ser Leu Ile
 645 650 655

Glu Glu Ser Pro Ile Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu
 660 665 670

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp
 675 680 685

Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly
 690 695 700

Leu Arg Ile Val Phe Val Val Leu Ser Ile Val Asn Arg Val Arg Gln
 705 710 715 720

Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Pro Arg Gly
 725 730 735

Pro Asp Arg Pro Glu Glu Ile Glu Glu Glu Gly Gly Asp Arg Asp Arg
 740 745 750

Asp Arg Ser Gly Leu Leu Val Asp Gly Phe Leu Thr Leu Ile Trp Val
 755 760 765

Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu
 770 775 780

Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
 785 790 795 800

Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu
 805 810 815

Leu Lys Asn Ser Ala Val Ser Leu Phe Asn Ala Thr Ala Ile Ala Val
 820 825 830

Ala Glu Gly Thr Asp Arg Val Ile Gln Val Leu Gln Arg Val Gly Arg
 835 840 845

Ala Leu Leu His Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala
850 855 860

Leu Leu
865

<210> 2
<211> 17
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> segment of R2 strain V3 domain

<400> 2
Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln
1 5 10 15

Ile

<210> 3
<211> 35
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> R2 strain V3 domain

<400> 3
Cys Ser Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro
1 5 10 15

Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln
20 25 30

Ala His Cys
35

<210> 4
<211> 35
<212> PRT
<213> Human immunodeficiency virus type 1

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<223> V3 domain of strain 93TH966.8

<400> 4

Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Thr Thr Ile Gly Pro
1 5 10 15

Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr Gly Asn Ile Arg Lys
20 25 30

Ala Tyr Cys
35

<210> 5

<211> 13

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: derivatives
of segment of V3 domain in R2 strain

<220>

<221> VARIANT

<222> (3)..(12)

<223> X = any natural or non-natural amino acid.

<400> 5

Pro Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln
1 5 10

<210> 6

<211> 30

<212> PRT

<213> Human immunodeficiency virus type 1

<220>

<223> sequence of Phenetic 1 in V3 region

<400> 6

Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15

Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 7

<211> 30

<212> PRT

<213> Human immunodeficiency virus type 1

<220>

<223> sequence of Phenetic 2 in V3 region

<400> 7

Asn Asn Thr Arg Lys Ser Ile Ser Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15

Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 8

<211> 30

<212> PRT

<213> Human immunodeficiency virus type 1

<220>

<223> sequence of Phenetic 3 in V3 region

<400> 8

Asn Asn Thr Arg Lys Ser Ile Ser Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15

Ala Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 9

<211> 30

<212> PRT

<213> Human immunodeficiency virus type 1

<220>

<223> sequence of Phenetic 4 in V3 region

<400> 9

Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr
1 5 10 15

Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 10
<211> 30
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 5 in V3 region

<400> 10
Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15
Ala Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 11
<211> 30
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 6 in V3 region

<400> 11
Lys Asn Thr Arg Arg Arg Ser His Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15
Thr Thr Lys Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 12
<211> 30
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> sequence of Phenetic 7 in V3 region

<400> 12
Asn Asn Thr Arg Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr
1 5 10 15
Arg Thr Gly Lys Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 13
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<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 8 in V3 region

<400> 13
Lys Lys Met Arg Thr Ser Ala Arg Ile Gly Pro Gly Arg Val Phe His
1 5 10 15

Lys Thr Gly Asp Ile Ile Gly Ser Ile Thr Lys Ala Tyr Cys
20 25 30

<210> 14
<211> 29
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 9 in V3 region

<400> 14
Asn Asn Thr Arg Gln Ser Thr His Ile Gly Pro Gly Gln Ala Leu Tyr
1 5 10 15

Thr Thr Asp Ile Ile Gly Lys Ile Arg Gln Ala His Cys
20 25

<210> 15
<211> 29
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 10 in V3 region

<400> 15
Asn Asn Thr Arg Gln Gly Thr His Ile Gly Pro Gly Arg Ala Tyr Tyr
1 5 10 15

Thr Thr Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys
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<210> 16
<211> 29
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> sequence of Phenetic 11 in V3 region

<400> 16
Asn Asn Thr Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Ala Leu Tyr
1 5 10 15

Thr Thr Glu Ile Arg Gly Asp Ile Arg Gln Ala Ala Cys
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<210> 17
<211> 30
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 12 in V3 region

<400> 17
Asp Asn Ile Lys Ile Gln Arg Thr Pro Ile Gly Gln Gly Gln Ala Leu
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Tyr Thr Thr Arg Ile Thr Gly Tyr Ile Gly Gln Ala His Cys
20 25 30

<210> 18
<211> 29
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Phenetic 13 in V3 region

<400> 18
Gln Asn Lys Arg Gln Gly Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr
1 5 10 15

Thr Thr Arg Ile Lys Gly Asp Ile Arg Lys Ala His Cys
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<210> 19
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<212> PRT
<213> Human immunodeficiency virus type 1
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<220>
<223> sequence of Clade A in V3 region

<400> 19
Asn Asn Thr Arg Lys Ser Val His Ile Gly Pro Gly Gln Ala Phe Tyr
1 5 10 15

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Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

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<210> 20
<211> 30
<212> PRT
<213> Human immunodeficiency virus type 1
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<220>
<223> sequence of Clade B in V3 region

<400> 20
Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr
1 5 10 15

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Thr Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

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<210> 21
<211> 30
<212> PRT
<213> Human immunodeficiency virus type 1
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<220>
<223> sequence of Clade C in V3 region

<400> 21
Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr
1 5 10 15

1
Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25 30

<210> 22
<211> 29
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Clade D in V3 region

<400> 22
Asn Asn Thr Arg Gln Arg Thr His Ile Gly Pro Gly Gln Ala Leu Tyr
1 5 10 15

Thr Thr Arg Ile Ile Gly Asp Ile Arg Gln Ala His Cys
20 25

<210> 23
<211> 30
<212> PRT
<213> Human immunodeficiency virus type 1

<220>
<223> sequence of Clade E in V3 region

<400> 23
Asn Asn Thr Arg Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr
1 5 10 15

Arg Thr Gly Asp Ile Ile Gly Asp Ile Arg Lys Ala Tyr Cys
20 25 30